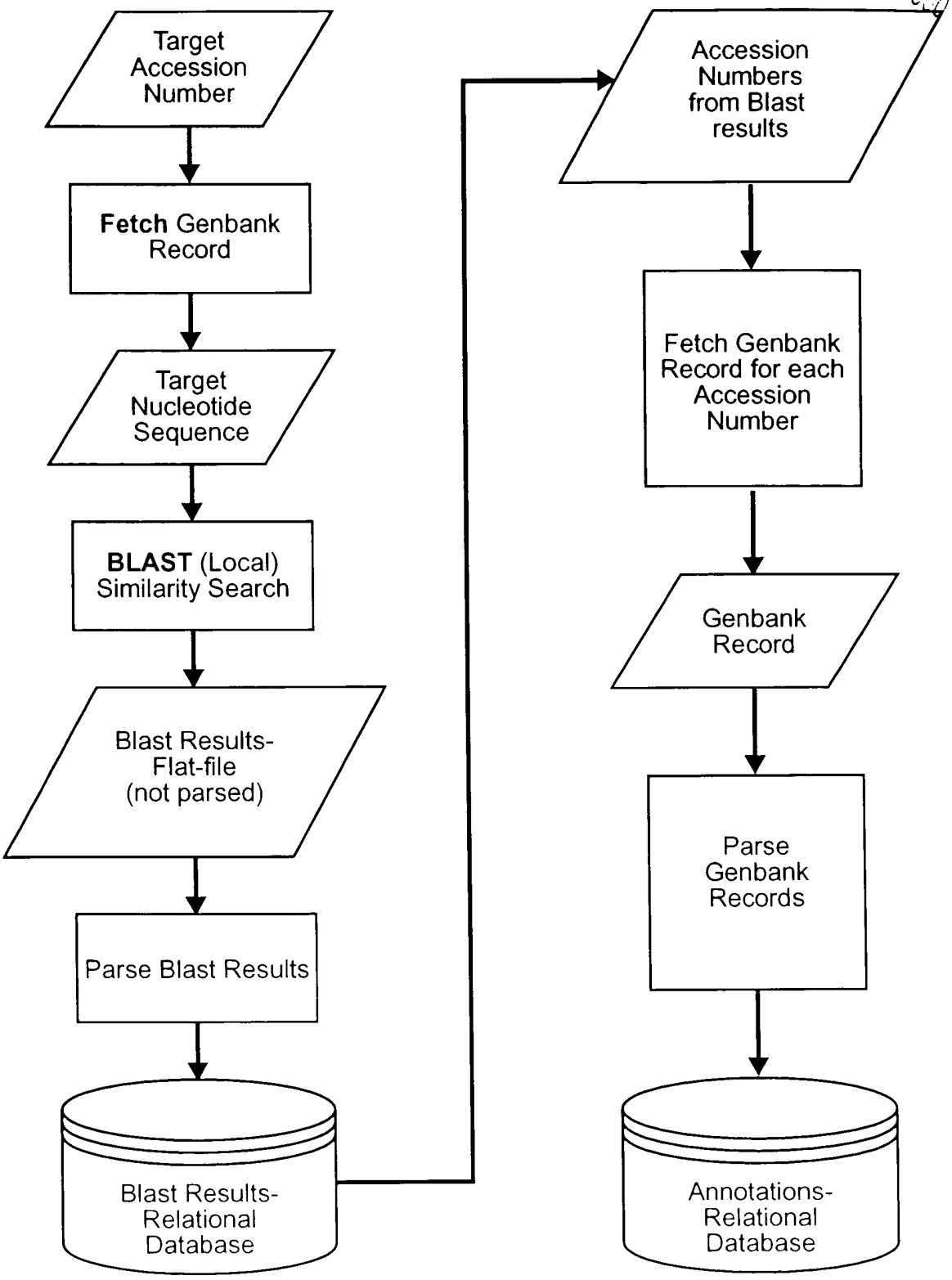


Figure 3

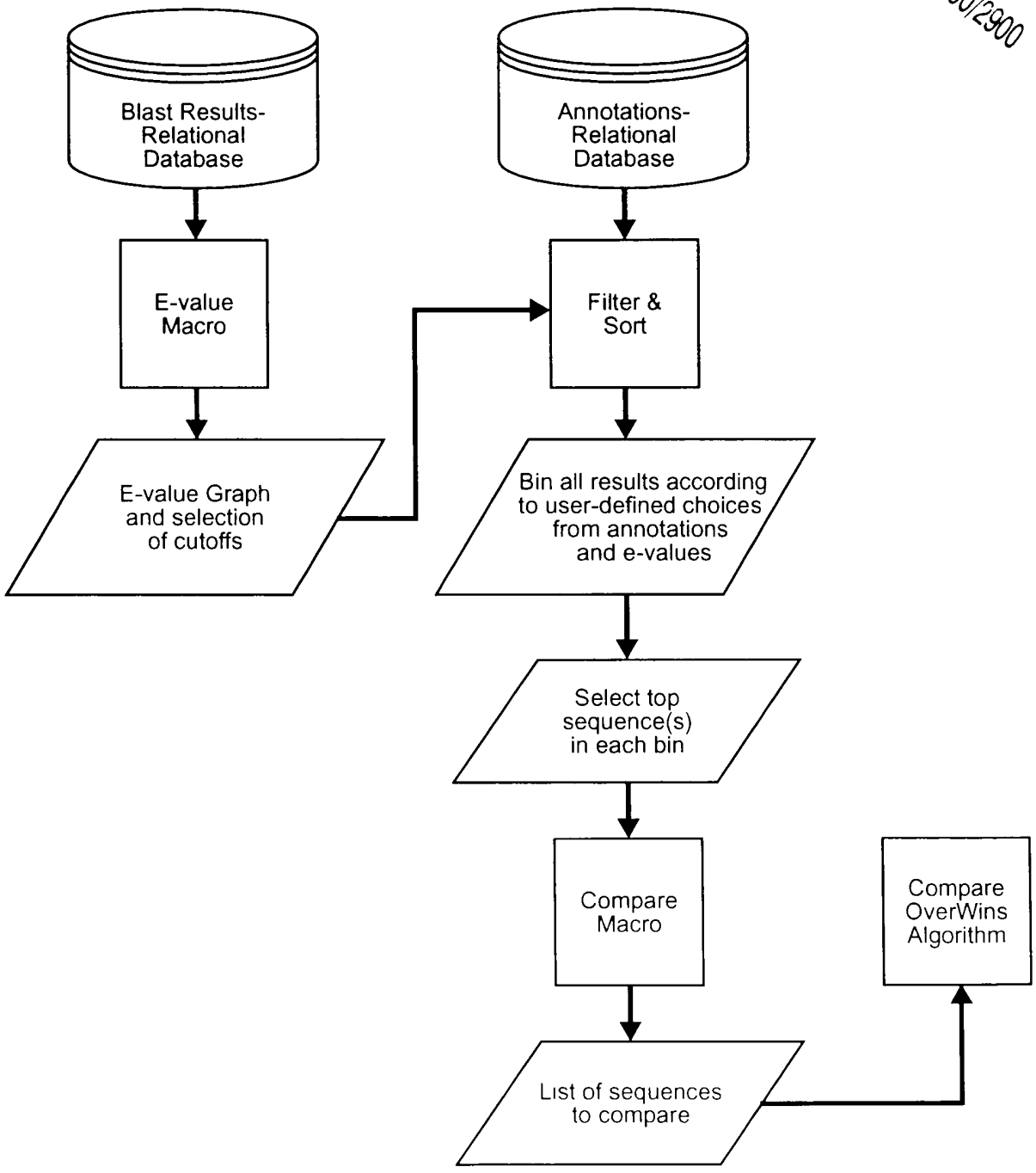


Figure 4

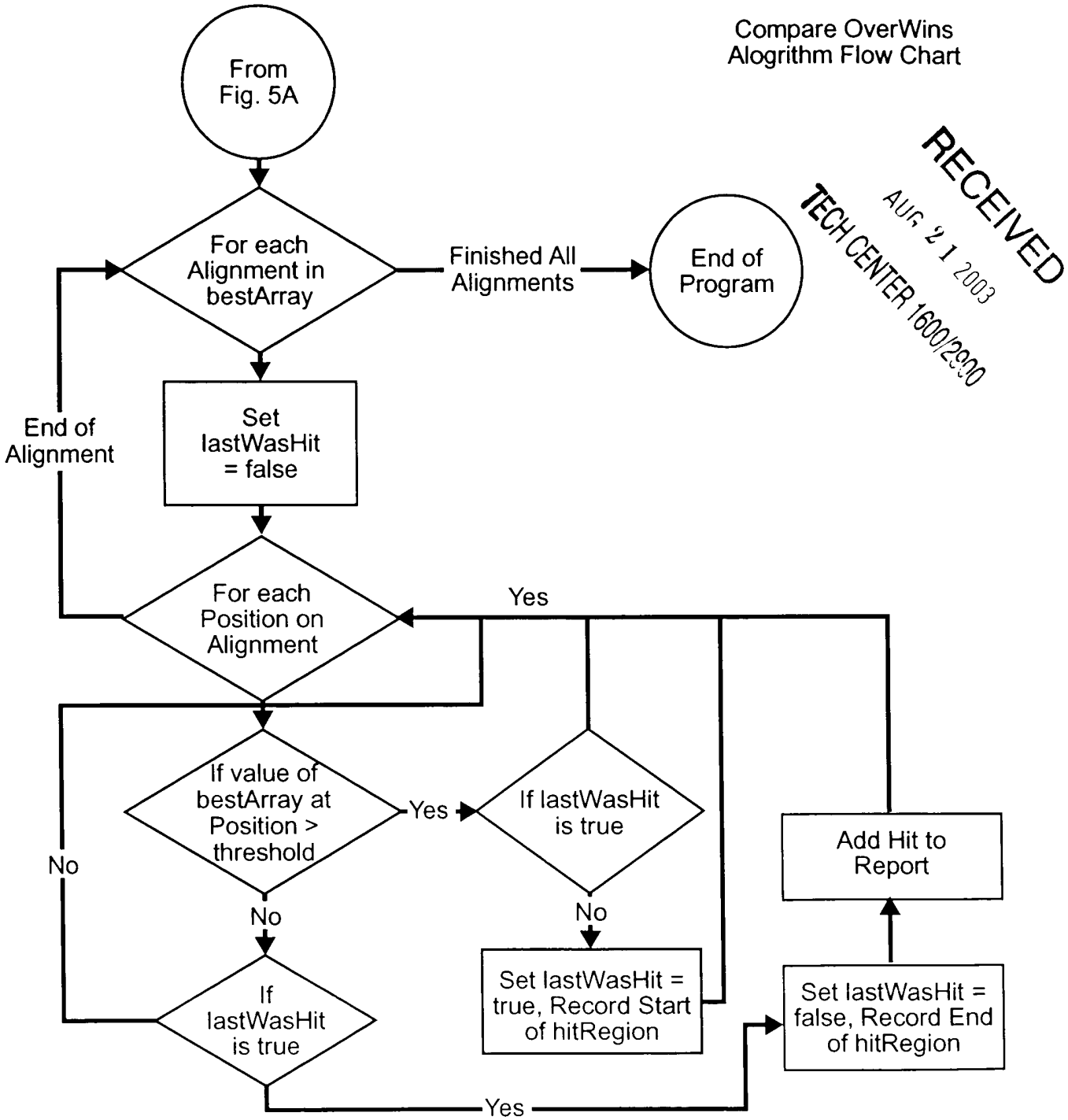


Figure 5B

Input:
Sequence A length a
Sequence B length b
Window Size

Output:
Array of size a by b of unsigned chars (0-255)
Each point represents the number of matches in the window at that alignment and position

Compare OverWins
Alogrithm Flow Chart
Basic Compare

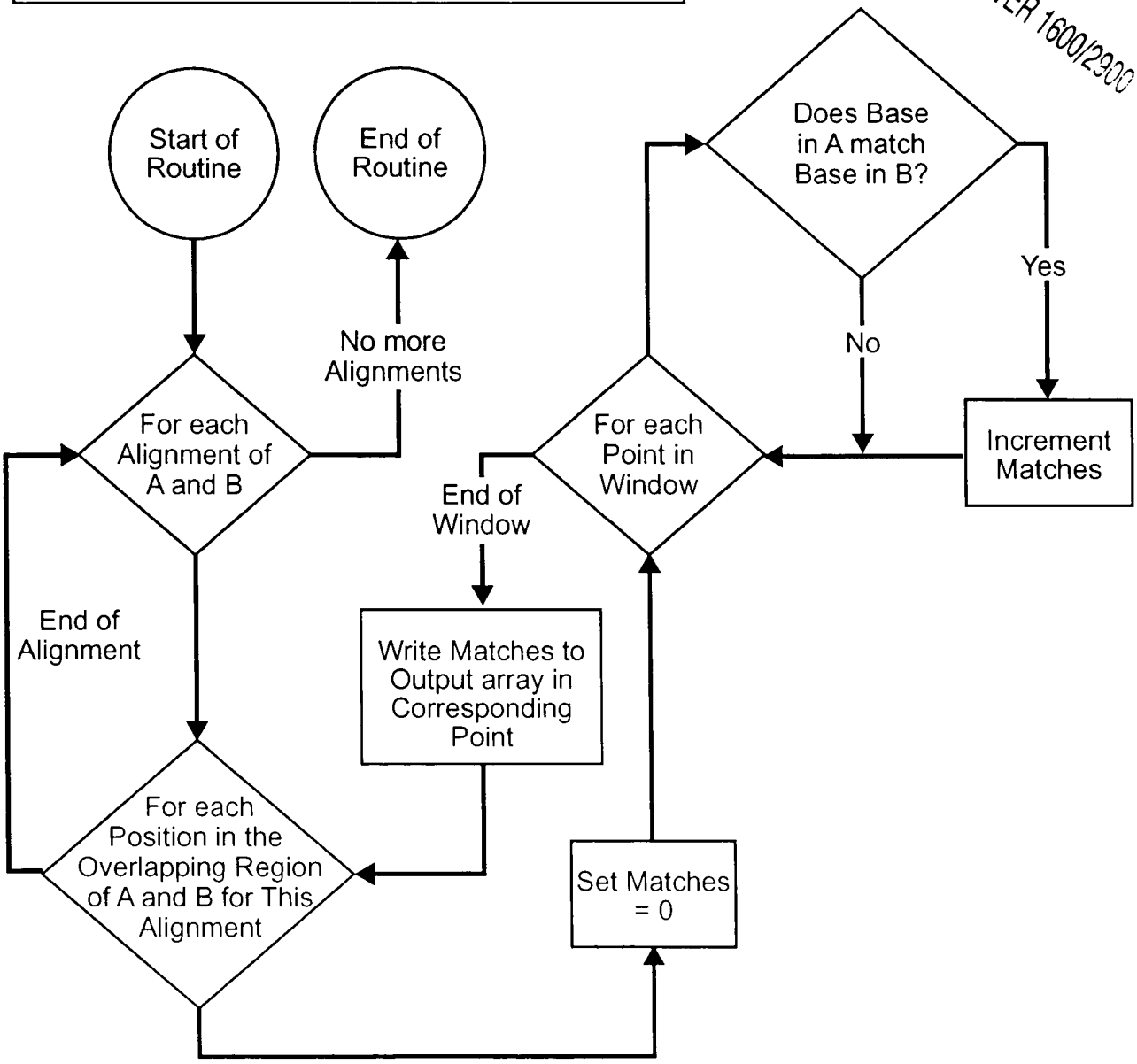


Figure 5C

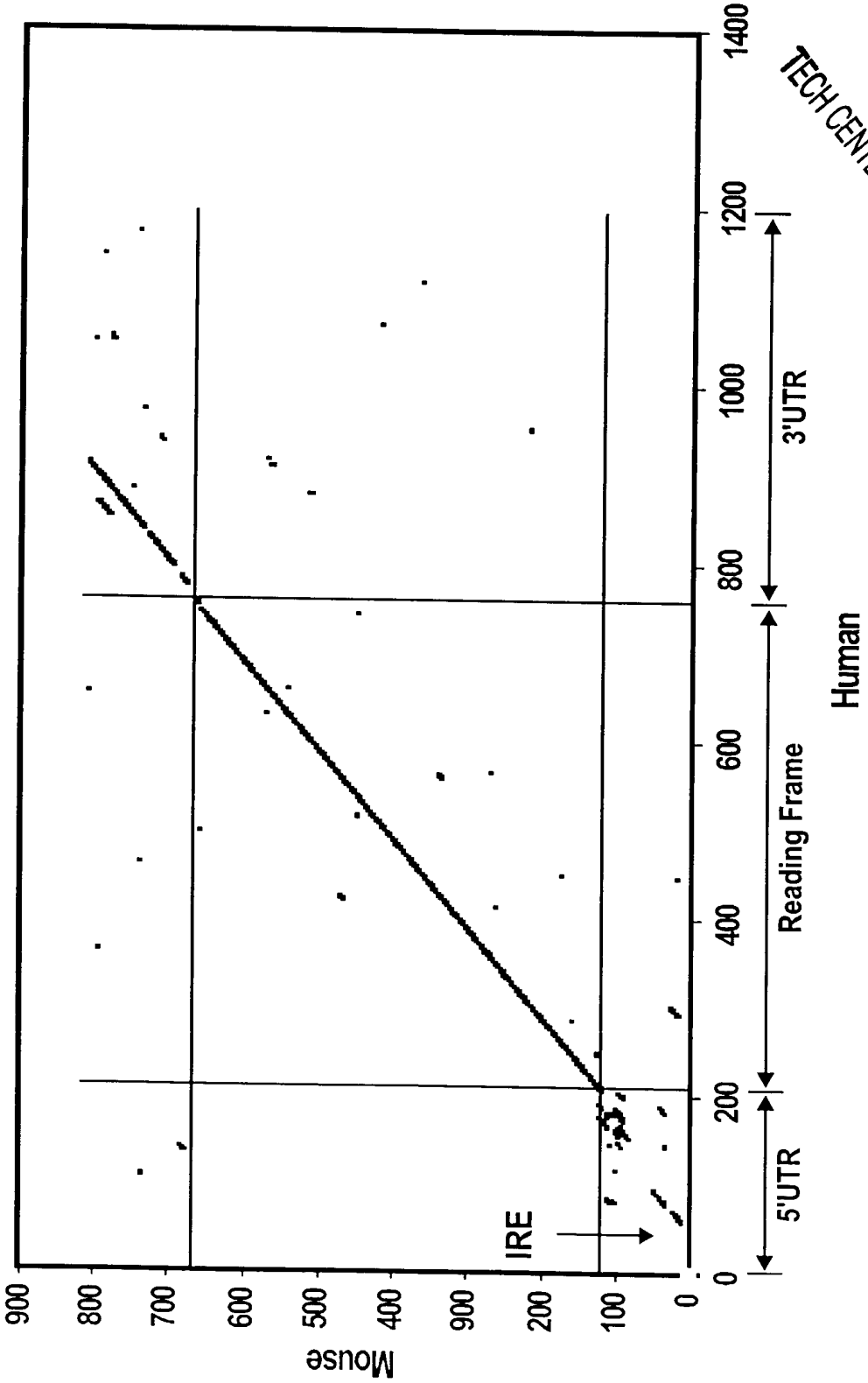


Figure 6

Self Complementation Analysis - Single Sequence

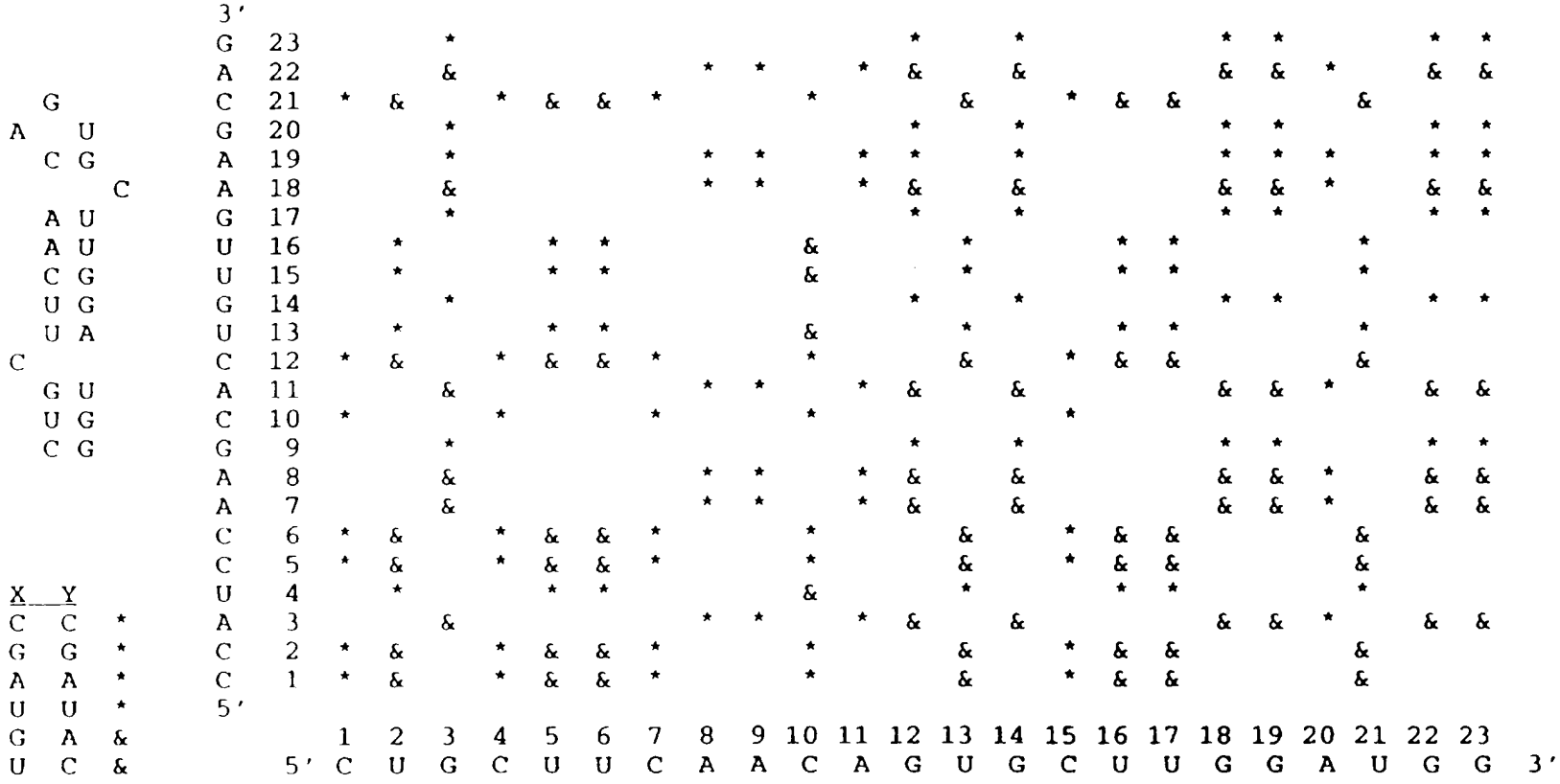


Figure 7

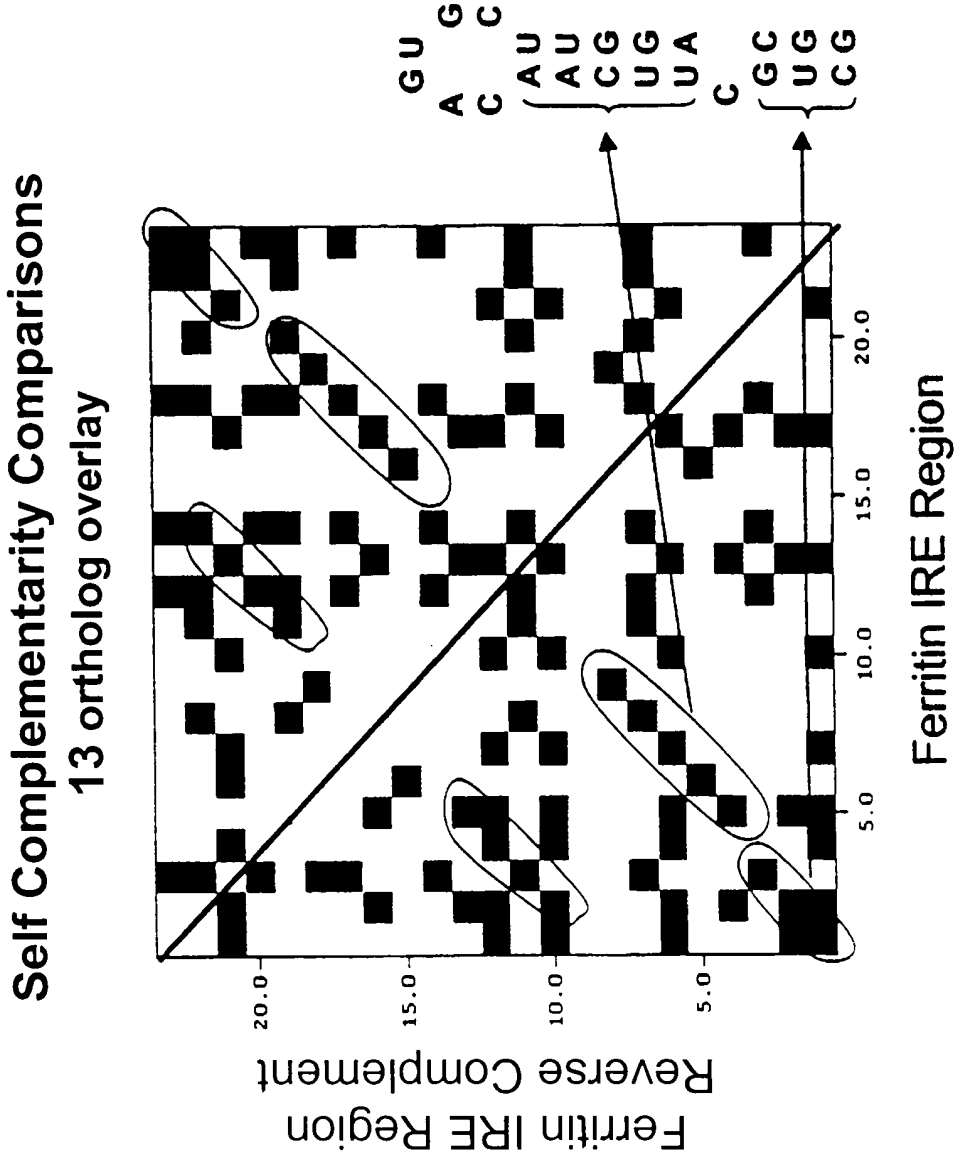
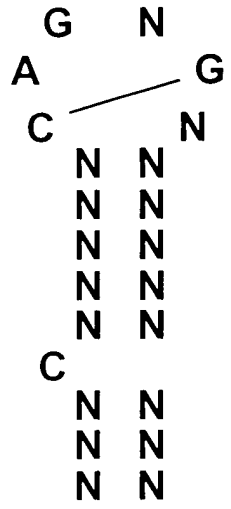


Figure 8



IRE
Stem-loop Model

```
H1  S1  H2  S2  H2  H1

H1  3:3  NNN:NNN
S1  1  C
H2  5:5  NNNNN:NNNNN
S2  6  CAGNGN

W2
M0
```

IRE String descriptor

This descriptor allows for
- a wobble (W) of 2
- no mismatches
- N can be any nucleotide
- H refers to the stem region
- S refers to the single stranded region

Figure 9

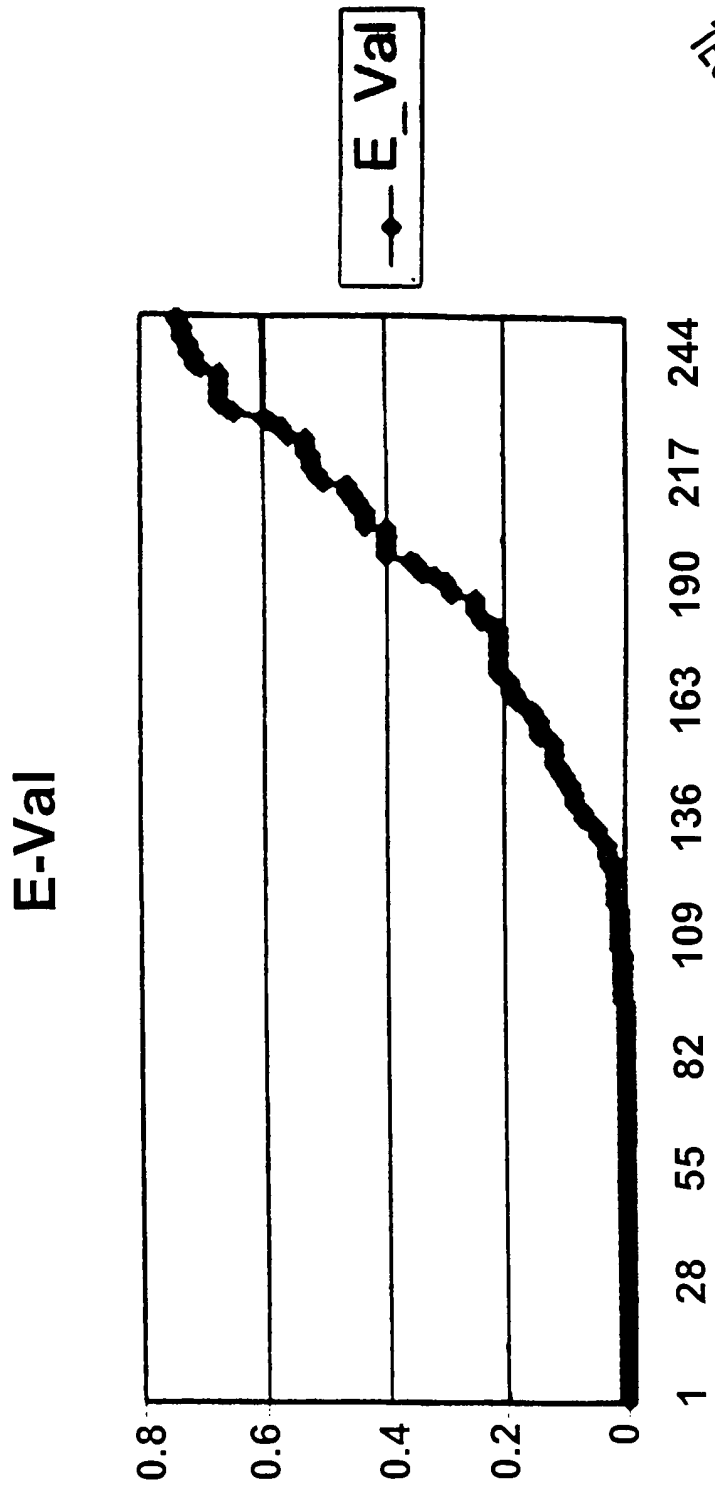


Figure 10

16S A Site rRNA

Control RNA

Figure 40

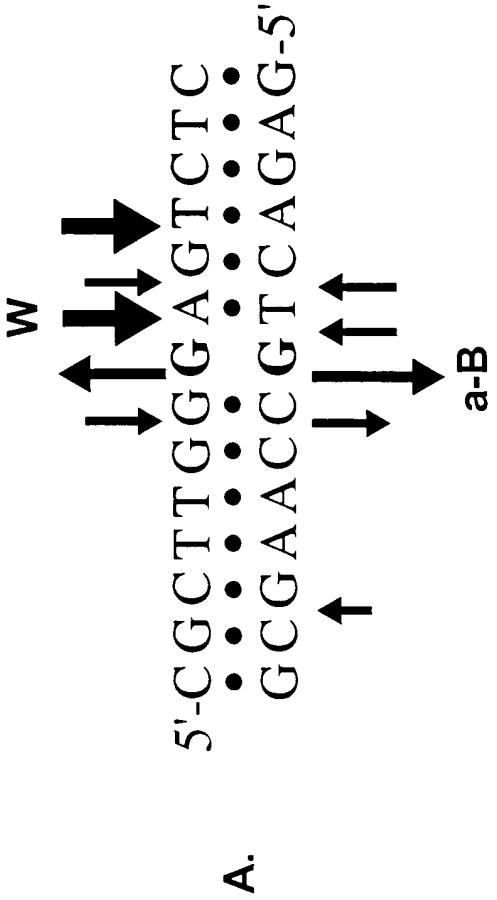


Figure 47

MS Fragmentation of DNA:RNA duplexes

Figure 48

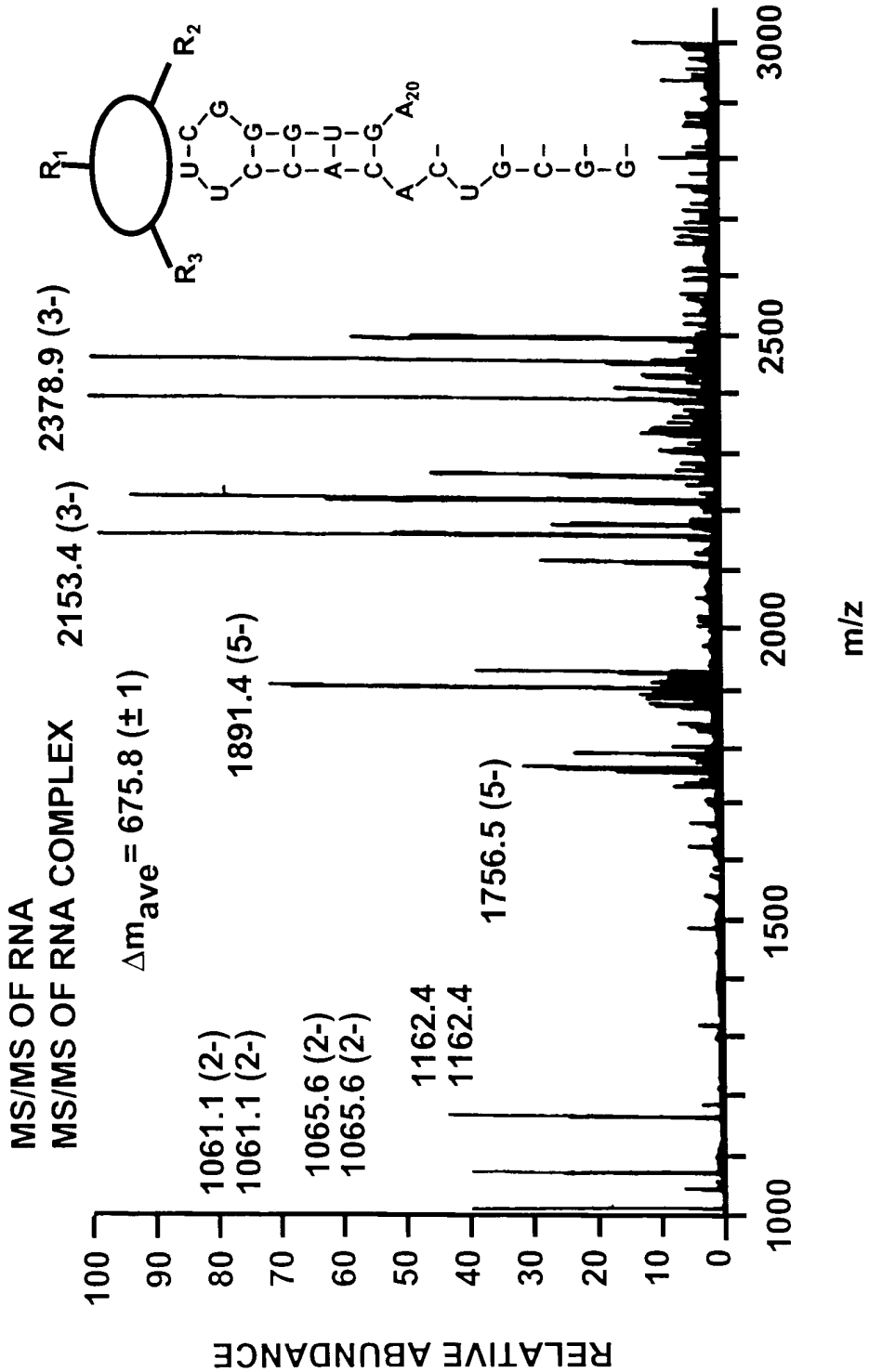


Figure 49

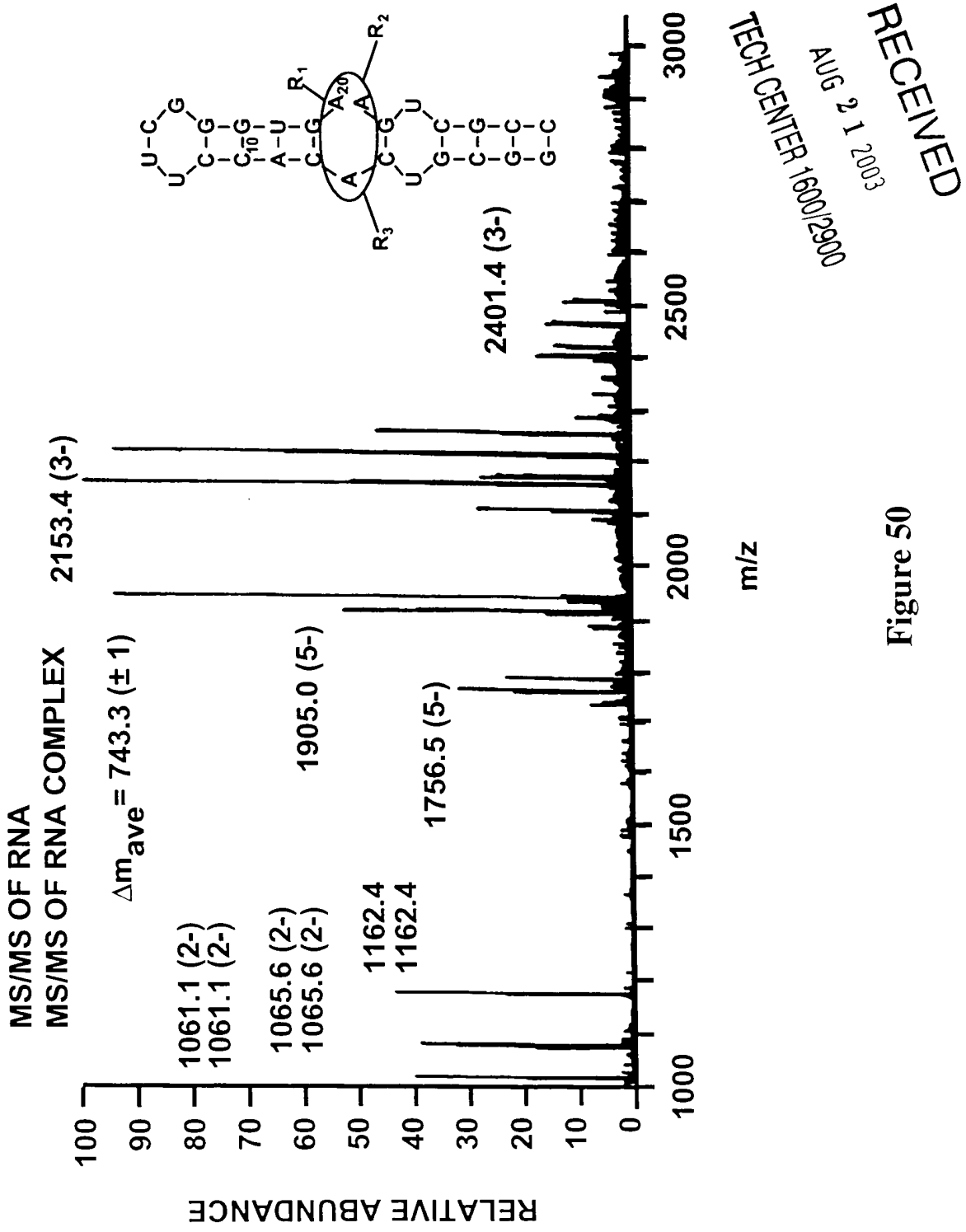


Figure 50